AMENDMENTS TO THE SPECIFICATION

Please replace paragraph [0015] with the following rewritten paragraph:

[0015] As used herein, the term "PRDT1 polypeptide" refers to a full-length PRDT1 protein or a fragment, derivative (variant), or ortholog thereof that is "functionally active," meaning that the protein fragment, derivative, or ortholog exhibits one or more or the functional activities associated with the polypeptide of SEQ ID NO:2. In one preferred embodiment, a functionally active PRDT1 polypeptide causes an altered pathogen resistance and drought tolerance phenotype when mis-expressed in a plant. In a further preferred embodiment, mis-expression of the functionally active PRDT1 polypeptide causes increased resistance to *P. parasitica* and/or other oomycetes and increased drought tolerance. In another embodiment, a functionally active PRDT1 polypeptide is capable of rescuing defective (including deficient) endogenous PRDT1 activity when expressed in a plant or in plant cells; the rescuing polypeptide may be from the same or from a different species as that with defective activity. In another embodiment, a functionally active fragment of a full length PRDT1 polypeptide (i.e., a native polypeptide having the sequence of SEQ ID NO:2 or a naturally occurring ortholog thereof) retains one of more of the biological properties associated with the full-length PRDT1 polypeptide, such as signaling activity, binding activity, catalytic activity, or cellular or extra-cellular localizing activity. Some preferred PRDT1 polypeptides display DNA binding activity. A PRDT1 fragment preferably comprises a PRDT1 domain, such as a C- or N-terminal or catalytic domain, among others, and preferably comprises at least 10, preferably at least 20, more preferably at least 25, and most preferably at least 50 contiguous amino acids of a PRDT1 protein. Functional domains can be identified using the PFAM program (Bateman A et al., 1999 Nucleic Acids Res 27:260-262~~; website at pfam.wustl.edu~~). A preferred PRDT1 fragment comprises a SANT domain (SM00395) identified by PFAM, at approximately amino acids 8-60. Functionally active variants of full-length PRDT1 polypeptides or fragments thereof include polypeptides with amino acid insertions, deletions, or substitutions that retain one of more of the biological properties associated with the full-length PRDT1 polypeptide. In some cases, variants are generated that change the post-translational processing of a PRDT1 polypeptide. For instance, variants may have altered protein transport or protein localization characteristics or altered protein half-life compared to the native polypeptide.

Please replace paragraph [0022] with the following rewritten paragraph:

[0022] As used herein, "percent (%) sequence identity" with respect to a specified subject sequence, or a specified portion thereof, is defined as the percentage of nucleotides or amino acids in the candidate derivative sequence identical with the nucleotides or amino acids in the subject sequence (or specified portion thereof), after aligning the sequences and introducing gaps, if necessary to achieve the maximum percent sequence identity, as generated by the program WU-BLAST-2.0a19 (Altschul *et al.*, J. Mol. Biol. (1990) 215:403-410~~; website at blast.wustl.edu/blast/README.html~~) with search parameters set to default values. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched. A "% identity value" is determined by the number of matching identical nucleotides or amino acids divided by the sequence length for which the percent identity is being reported. "Percent (%) amino acid sequence similarity" is determined by doing the same calculation as for determining % amino acid sequence identity, but including conservative amino acid substitutions in addition to identical amino acids in the computation. A conservative amino acid substitution is one in which an amino acid is substituted for another amino acid having similar properties such that the folding or activity of the protein is not significantly affected. Aromatic amino acids that can be substituted for each other are phenylalanine, tryptophan, and tyrosine; interchangeable hydrophobic amino acids are leucine, isoleucine, methionine, and valine; interchangeable polar amino acids are glutamine and asparagine; interchangeable basic amino acids are arginine, lysine and histidine; interchangeable acidic amino acids are aspartic acid and glutamic acid; and interchangeable small amino acids are alanine, serine, threonine, cysteine and glycine.

Please replace paragraph [0051] with the following rewritten paragraph:

[0051] The sequence flanking the right T-DNA border was subjected to a basic BLASTN search and/or a search of the *Arabidopsis* Information Resource (TAIR) database ~~(available at the arabidopsis.org website)~~, which revealed sequence identity to BAC F22H5, (GI 12331602), mapped to chromosome 1. The junction of the left border of the T-DNA is at nt 20167 of F22H5, and the right border junction is at nt 20229. Sequence analysis revealed that the T-DNA had inserted in the vicinity (*i.e.*, within about 10 kb) of the gene whose nucleotide sequence is presented

as SEQ ID NO: 1 (GI 18410812 and GI 12331602, nucleotides 20955 – 21335) and which we designated PRDT1. Specifically, the right border was approximately 500 bp upstream of the start codon of SEQ ID NO:1.